Fig. 1

```
          10          20          30          40          50          60
ATG GCC GCA GAG GCG ACG TTG GGT CCG AAC GTG AGC TGG TGG GCT CCG TCC AAC GCT TCG
Met Ala Ala Glu Ala Thr Leu Gly Pro Asn Val Ser Trp Trp Ala Pro Ser Asn Ala Ser

          70          80          90          100         110         120
GGA TGC CCG GGC TGC GGT GTC AAT GCC TCG GAT GGC CCA GGC TCC GCG CCA AGG CCC CTG
Gly Cys Pro Gly Cys Gly Val Asn Ala Ser Asp Gly Pro Gly Ser Ala Pro Arg Pro Leu

          130         140         150         160         170         180
GAT GCC TGG CTG GTG CCC CTG TTT TTC GCT GCC CTA ATG TTG CTG GGG CTA GTC GGG AAC
Asp Ala Trp Leu Val Pro Leu Phe Phe Ala Ala Leu Met Leu Leu Gly Leu Val Gly Asn

          190         200         210         220         230         240
TCA CTG GTC ATC TTC GTT ATC TGC CGC CAC AAG CAC ATG CAG ACC GTC ACC AAT TTC TAC
Ser Leu Val Ile Phe Val Ile Cys Arg His Lys His Met Gln Thr Val Thr Asn Phe Tyr

          250         260         270         280         290         300
ATC GCT AAC CTG GCG GCC ACA GAT GTC ACT TTC CTT CTG TGC TGC GTA CCC TTC ACC GCG
Ile Ala Asn Leu Ala Ala Thr Asp Val Thr Phe Leu Leu Cys Cys Val Pro Phe Thr Ala

          310         320         330         340         350         360
CTC CTC TAT CCG CTG CCC ACC TGG GTG CTG GGA GAC TTC ATG TGC AAA TTC GTC AAC TAC
Leu Leu Tyr Pro Leu Pro Thr Trp Val Leu Gly Asp Phe Met Cys Lys Phe Val Asn Tyr

          370         380         390         400         410         420
ATC CAG CAG GTC TCG GTG CAA GCC ACA TGT GCC ACT TTG ACA GCC ATG AGT GTG GAC CGC
Ile Gln Gln Val Ser Val Gln Ala Thr Cys Ala Thr Leu Thr Ala Met Ser Val Asp Arg
```

Fig. 2

```
          430         440         450         460         470         480
TGG TAC GTG ACT GTG TTC CCG CTG CGT GCA CTT CAC CGC CGC ACT CCG CGC CTG GCC CTG
Trp Tyr Val Thr Val Phe Pro Leu Arg Ala Leu His Arg Arg Thr Pro Arg Leu Ala Leu

          490         500         510         520         530         540
ACT GTC AGC CTT AGC ATC TGG GTG GGT TCC GCA GCT GTT TCC GCC CCG GTG CTG GCT CTG
Thr Val Ser Leu Ser Ile Trp Val Gly Ser Ala Ala Val Ser Ala Pro Val Leu Ala Leu

          550         560         570         580         590         600
CAC CGC CTG TCG CCC GGG CCT CAC ACC TAC TGC AGT GAG GCG TTT CCC AGC CGT GCC CTG
His Arg Leu Ser Pro Gly Pro His Thr Tyr Cys Ser Glu Ala Phe Pro Ser Arg Ala Leu

          610         620         630         640         650         660
GAG CGC GCT TTC GCG CTC TAC AAC CTG CTG GCC CTA TAC CTG CTG CCG CTG CTC GCC ACC
Glu Arg Ala Phe Ala Leu Tyr Asn Leu Leu Ala Leu Tyr Leu Leu Pro Leu Leu Ala Thr

          670         680         690         700         710         720
TGC GCC TGC TAC GGT GCC ATG CTG CGC CAC CTG GGC CGC GCC GCT GTA CGC CCC GCA CCC
Cys Ala Cys Tyr Gly Ala Met Leu Arg His Leu Gly Arg Ala Ala Val Arg Pro Ala Pro

          730         740         750         760         770         780
ACT GAT GGC GCC CTG CAG GGG CAG CTG CTA GCA CAG CGC GCT GGA GCA GTG CGC ACC AAG
Thr Asp Gly Ala Leu Gln Gly Gln Leu Leu Ala Gln Arg Ala Gly Ala Val Arg Thr Lys

          790         800         810         820         830         840
GTC TCC CGG CTG GTG GCC GCT GTC GTC CTG CTC TTC GCC GCC TGC TGG GGC CCG ATC CAG
Val Ser Arg Leu Val Ala Ala Val Val Leu Leu Phe Ala Ala Cys Trp Gly Pro Ile Gln

          850         860         870         880         890         900
CTG TTC CTG GTG CTT CAA GCC CTG GGC CCC TCG GGG GCC TGG CAC CCT CGA AGC TAT GCC
Leu Phe Leu Val Leu Gln Ala Leu Gly Pro Ser Gly Ala Trp His Pro Arg Ser Tyr Ala
```

Fig. 3

```
          910         920         930         940         950         960
GCC TAC GCG CTC AAG ATC TGG GCT CAC TGC ATG TCC TAC AGC AAT TCT GCG CTC AAC CCG
Ala Tyr Ala Leu Lys Ile Trp Ala His Cys Met Ser Tyr Ser Asn Ser Ala Leu Asn Pro

          970         980         990        1000        1010        1020
CTG CTC TAT GCC TTC CTG GGT TCC CAC TTC AGA CAG GCC TTC TGC CGC GTG TGC CCC TGC
Leu Leu Tyr Ala Phe Leu Gly Ser His Phe Arg Gln Ala Phe Cys Arg Val Cys Pro Cys

         1030        1040        1050        1060        1070        1080
GGC CCG CAA CGC CAG CGT CGG CCC CAC GCG TCA GCG CAC TCG GAC CGA GCC GCA CCC CAT
Gly Pro Gln Arg Gln Arg Arg Pro His Ala Ser Ala His Ser Asp Arg Ala Ala Pro His

         1090        1100        1110        1120        1130        1140
AGT GTG CCG CAC AGC CGG GCT GCG CAC CCT GTC CGG GTC AGG ACC CCC GAG CCT GGG AAC
Ser Val Pro His Ser Arg Ala Ala His Pro Val Arg Val Arg Thr Pro Glu Pro Gly Asn

         1150        1160        1170        1180        1190        1200
CCT GTG GTG CGC TCG CCC TCT GTT CAG GAT GAA CAC ACT GCC CCA CTC TGA
Pro Val Val Arg Ser Pro Ser Val Gln Asp Glu His Thr Ala Pro Leu ***
```

Fig. 4

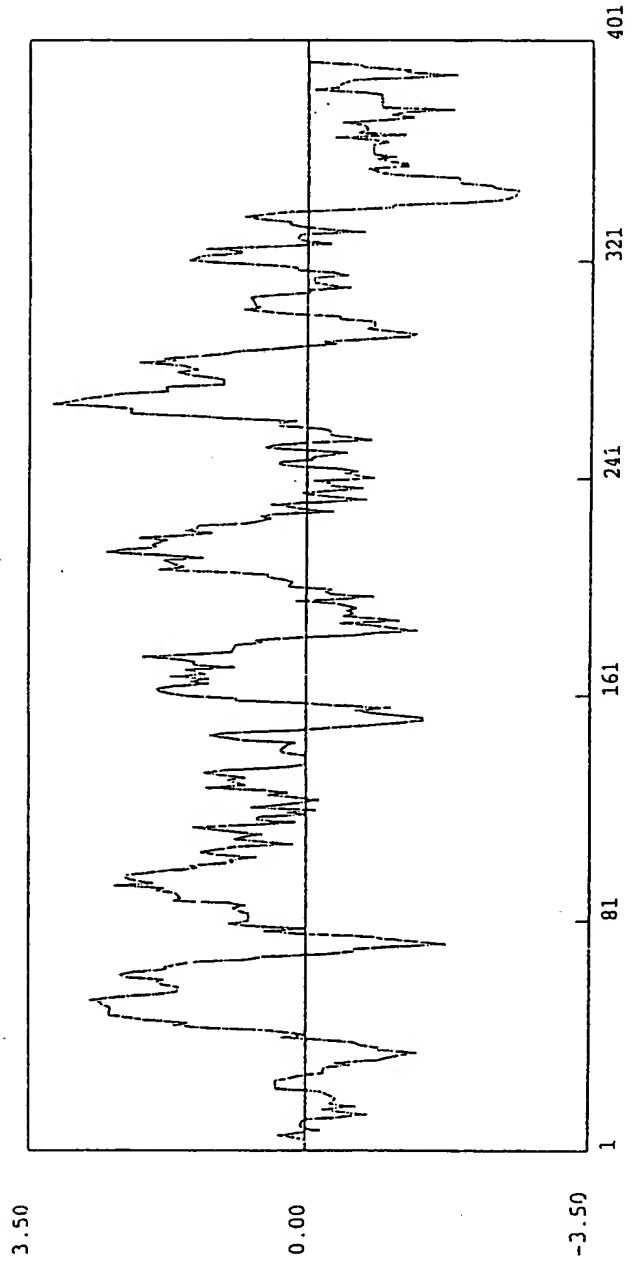


Fig. 5

```
        10         20         30         40         50         60
ATGCACACCG TGGCTACGTC CGGACCCAAC GCGTCCTGGG GGGCACCGGC CAACGCCTCC
METHisThrV alAlaThrSe rGlyProAsn AlaSerTrpG lyAlaProAl aAsnAlaSer

        70         80         90        100        110        120
GGCTGCCCGG GCTGTGGCGC CAACGCCTCG GACGGCCCAG TCCCTTCGCC GCGGGCCGTG
GlyCysProG lyCysGlyAl aAsnAlaSer AspGlyProV alProSerPr oArgAlaVal

       130        140        150        160        170        180
GACGCCTGGC TCGTGCCGCT CTTCTTCGCG GCGCTGATGC TGCTGGGCCT GGTGGGGAAC
AspAlaTrpL euValProLe uPhePheAla AlaLeuMETL euLeuGlyLe uValGlyAsn

       190        200        210        220        230        240
TCGCTGGTCA TCTACGTCAT CTGCCGCCAC AAGCCGATGC GGACCGTGAC CAACTTCTAC
SerLeuVall leTyrVallI eCysArgHis LysProMETA rgThrValTh rAsnPheTyr

       250        260        270        280        290        300
ATCGCCAACC TGGCGGCCAC GGACGTGACC TTCCTCCTGT GCTGCGTCCC CTTCACGGCC
IleAlaAsnL euAlaAlaTh rAspValThr PheLeuLeuC ysCysValPr oPheThrAla

       310        320        330        340        350        360
CTGCTGTACC CGCTGCCCGG CTGGGTGCTG GGCGACTTCA TGTGCAAGTT CGTCAACTAC
LeuLeuTyrP roLeuProGl yTrpValLeu GlyAspPheM ETCysLysPh eValAsnTyr

       370        380        390        400        410        420
ATCCAGCAGG TCTCGGTGCA GGCCACGTGT GCCACTCTGA CCGCCATGAG TGTGGACCGC
IleGlnGlnV alSerValGl nAlaThrCys AlaThrLeuT hrAlaMETSe rValAspArg
```

Fig. 6

```
       430        440        450        460        470        480
TGGTACGTGA CGGTGTTCCC GTTGCGCGCC CTGCACCGCC GCACGCCCCG CCTGGCGCTG
TrpTyrValT hrValPhePr oLeuArgAla LeuHisArgA rgThrProAr gLeuAlaLeu

       490        500        510        520        530        540
GCTGTCAGCC TCAGCATCTG GGTAGGCTCT GCGGCGGTGT CTGCGCCGGT GCTCGCCCTG
AlaValSerL euSerIleTr pValGlySer AlaAlaValS erAlaProVa lLeuAlaLeu

       550        560        570        580        590        600
CACCGCCTGT CACCCGGGCC GCGCGCCTAC TGCAGTGAGG CCTTCCCCAG CCGCGCCCTG
HisArgLeuS erProGlyPr oArgAlaTyr CysSerGluA laPheProSe rArgAlaLeu

       610        620        630        640        650        660
GAGCGCGCCT TCGCACTGTA CAACCTGCTG GCGCTGTACC TGCTGCCGCT GCTCGCCACC
GluArgAlaP heAlaLeuTy rAsnLeuLeu AlaLeuTyrL euLeuProLe uLeuAlaThr

       670        680        690        700        710        720
TGCGCCTGCT ATGCGGCCAT GCTGCGCCAC CTGGGCCGGG TCGCCGTGCG CCCCGCGCCC
CysAlaCysT yrAlaAlaME TLeuArgHis LeuGlyArgV alAlaValAr gProAlaPro

       730        740        750        760        770        780
GCCGATAGCG CCCTGCAGGG GCAGGTGCTG GCAGAGCGCG CAGGCGCCGT GCGGGCCAAG
AlaAspSerA laLeuGlnGl yGlnValLeu AlaGluArgA laGlyAlaVa lArgAlaLys
```

Fig. 7

```
      790        800        810        820        830        840
GTCTCGCGGC TGGTGGCGGC CGTGGTCCTG CTCTTCGCCG CCTGCTGGGG CCCCATCCAG
ValSerArgL euValAlaAl aValValLeu LeuPheAlaA laCysTrpGl yProIleGln

      850        860        870        880        890        900
CTGTTCCTGG TGCTGCAGGC GCTGGGCCCC GCGGGCTCCT GGCACCCACG CAGCTACGCC
LeuPheLeuV alLeuGlnAl aLeuGlyPro AlaGlySerT rpHisProAr gSerTyrAla

      910        920        930        940        950        960
GCCTACGCGC TTAAGACCTG GGCTCACTGC ATGTCCTACA GCAACTCCGC GCTGAACCCG
AlaTyrAlaL euLysThrTr pAlaHisCys METSerTyrS erAsnSerAl aLeuAsnPro

      970        980        990       1000       1010       1020
CTGCTCTACG CCTTCCTGGG CTCGCACTTC CGACAGGCCT TCCGCCGCGT CTGCCCCTGC
LeuLeuTyrA laPheLeuGl ySerHisPhe ArgGlnAlaP heArgArgVa lCysProCys

      1030       1040       1050       1060       1070       1080
GCGCCGCGCC GCCCCCGCCG CCCCCGCCGG CCCGGACCCT CGGACCCCGC AGCCCCACAC
AlaProArgA rgProArgAr gProArgArg ProGlyProS erAspProAl aAlaProHis

      1090       1100       1110       1120       1130       1140
GCGGAGCTGC ACCGCCTGGG GTCCCACCCG GCCCCCGCCA GGGCGCAGAA GCCAGGGAGC
AlaGluLeuH isArgLeuGl ySerHisPro AlaProAlaA rgAlaGlnLy sProGlySer

      1150       1160       1170       1180       1190       1200
AGTGGGCTGG CCGCGCGCGG GCTGTGCGTC CTGGGGGAGG ACAACGCCCC TCTCTGA
SerGlyLeuA laAlaArgGl yLeuCysVal LeuGlyGluA spAsnAlaPr oLeu***
```

Fig. 8

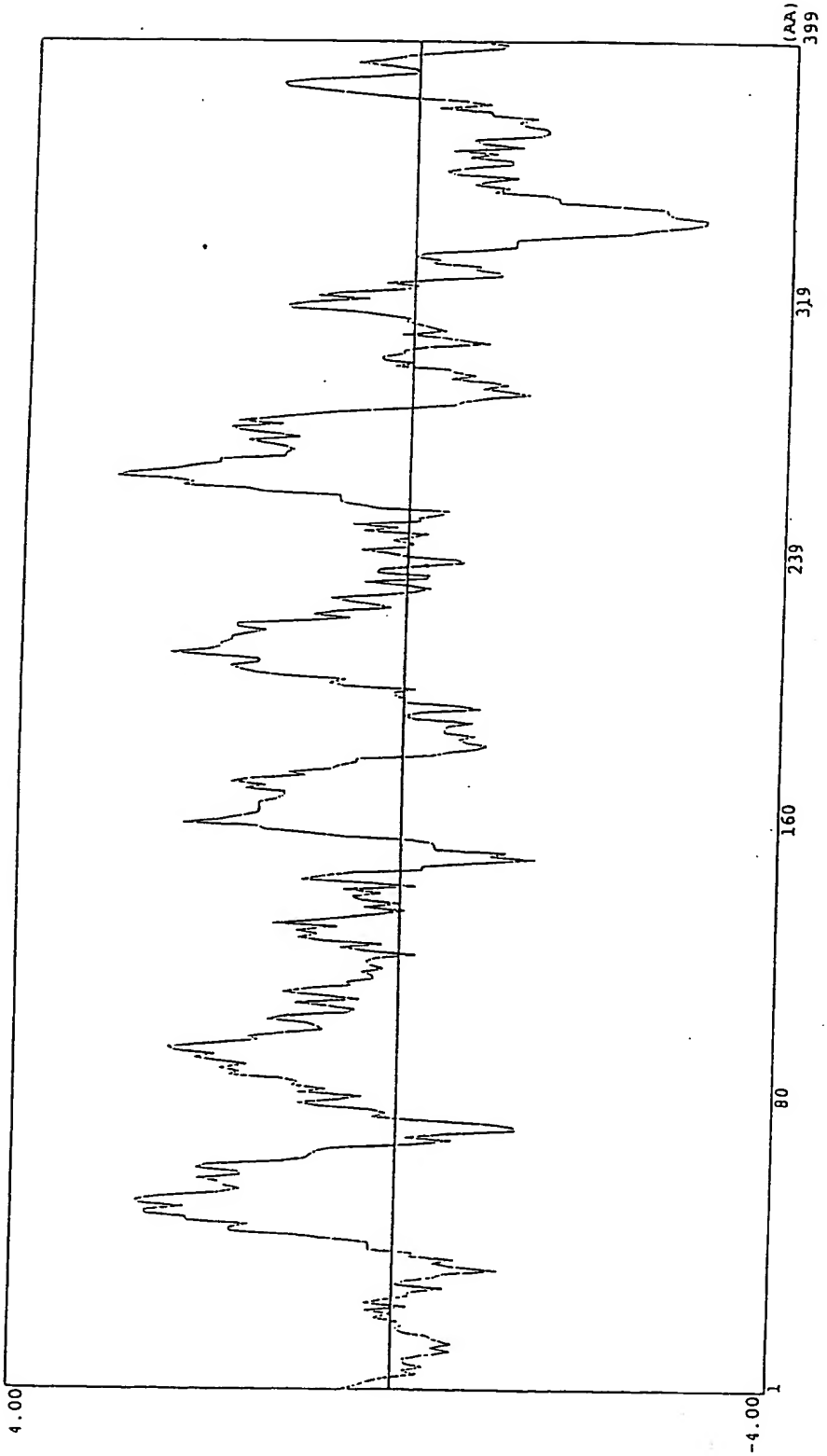
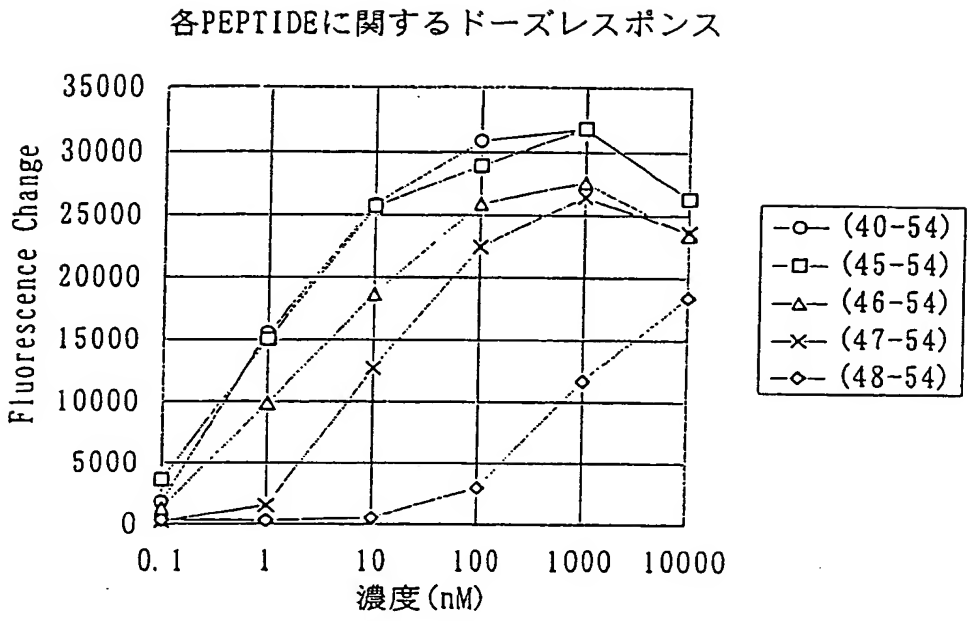


Fig. 9


各PEPTIDEに関するドーズレスポンス
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20000
15000
10000
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100
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濃度(nM)
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